SEQUENCE LISTING

<110>   Glassman, Kimberly F.
         Gordon-Kamm, William J.
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         Stecca, Kevin L.

<120>   RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION

<130>   BB1449 US NA

<140>   US/09/887,194
<141>   2001-06-22

<160>   36

<170>   Microsoft Office 97

<210>   1
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<220>
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<400>   1
gaattcgcgg ccgcatggga ggtagaggtc   30

<210>   2
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<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence: PCR primer for amplification
         of soybean Fad2-1

<400>   2
ggaaaaccat gcaacccatt ggtacttgct   30

<210>   3
<211>   30
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence: PCR primer for amplification
         of soybean Fad2-1

<400>   3
agcaagtacc aatgggttgc atggtttttcc   30

<210>   4
<211>   30

1

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<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence:  PCR primer for amplification
       of soybean Fad2-1

<400>  4
agcaagtacc aatggatact tgttcctgta                              30


<210>  5
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<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence:  PCR primer for amplification
       of soybean Fad2-1

<400>  5
tacaggaaca agtatccatt ggtacttgct                              30


<210>  6
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence:  pKS102 linker

<400>  6
gaattcgcgg ccgcatggga ggtagaggtc                              30


<210>  7
<211>  34
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence:  PCR primer for amplification
       of Cer3

<400>  7
ggcgcgccaa gcttggatcc gtcgacggcg cgcc                         34


<210>  8
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence:  PCR primer for amplification
       of Cer3

<400>  8
gaattcgcgg ccgcggcacg agatttgagg                              30
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2

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<210>  9
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence:  PCR primer for amplification
       of Cer3

<400>  9
ttgcccaatg tttatgcata tgtagaactg                                    30


<210>  10
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence:  PCR primer for amplification
       of Cer3

<400>  10
cagttctaca tatgcataaa cattgggcaa                                    30


<210>  11
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence:  ELVISLIVES complementary
       region of pKS106 and pKS124

<400>  11
gaattcgcgg ccgcggcacg agatttgagg                                    30


<210>  12
<211>  80
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence:  ELVISLIVES complementary
       region of pKS106 and pKS124

<400>  12
cggccggagc tggtcatctc gctcatcgtc gagtcggcgg ccgccgactc gacgatgagc 60
gagatgacca gctccggccg                                               80


<210>  13
<211>  154
<212>  DNA
<213>  Artificial Sequence
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3

<220>
<223> Description of Artificial Sequence: ELVISLIVES complementary
       region of pKS133

<400> 13
cggccggagc tggtcatctc gctcatcgtc gagtcggcgg ccggagctgg tcatctcgct 60
catcgtcgag tcggcggccg ccgactcgac gatgagcgag atgaccagct ccggccgccg 120
actcgacgat gagcgagatg accagctccg gccg   154

<210> 14
<211> 92
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: ELVISLIVES PCR primer

<400> 14
gaattccggc cggagctggt catctcgctc atcgtcgagt cggcggccgc cgactcgacg 60
atgagcgaga tgaccagctc cggccggaat tc   92

<210> 15
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: ELVISLIVES PCR primer

<400> 15
gaattccggc cggag   15

<210> 16
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer for amplification
       of soybean Fad2-1

<400> 16
gaattcgcgg ccgctgagtg attgctcacg agt   33

<210> 17
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer for amplification
       of soybean Fad2-1

<400> 17
gaattcgcgg ccgcttaatc tctgtccata gtt   33

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<210>  18
<211>  32
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence:  PCR primer for amplification
       of soybean Fad2-1, 5'-end

<400>  18
gaattcgcgg ccgcccaatc tattgggttc tc                              32


<210>  19
<211>  32
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence:  PCR primer for amplification
       of soybean Fad2-1, 3'-end of 25 nucleotide fragment

<400>  19
gaattcgcgg ccgcaacctt ggagaaccca at                              32


<210>  20
<211>  32
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence:  PCR primer for amplification
       of soybean Fad2-1, 3'-end 75 nucleotide fragment

<400>  20
gaattcgcgg ccgcggcatg gtgaccacac tc                              32


<210>  21
<211>  32
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence:  PCR primer for amplification
       of soybean Fad2-1, 3'-end of 150 nucleotide fragment

<400>  21
gaattcgcgg ccgctgagaa ataagggact aa                              32


<210>  22
<211>  32
<212>  DNA
<213>  Artificial Sequence
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<220>
<223> Description of Artificial Sequence: PCR primer for amplification
of soybean Fad2-1, 3'-end 300 nucleotide fragment

<400> 22
gaattcgcgg ccgcgagtgt gacgagaaga ga   32

<210> 23
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer for amplification
of soybean Fad2-1, 3'-end 600 nucleotide fragment

<400> 23
gaattcgcgg ccgcttctga tgaatcgtaa tg   32

<210> 24
<211> 1717
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: ELVISLIVES complementary
region of pBS68

<400> 24
cggccggagc tggtcatctc gctcatcgtc gagtcggcgg ccgctgagtg attgctcacg   60
agtgtggtca ccatgccttc agcaagtacc aatgggttga tgatgttgtg ggtttgaccc 120
ttcactcaac acttttagtc ccttatttct catggaaaat aagccatcgc cgccatcact 180
ccaacacagg ttcccttgac cgtgatgaag tgtttgtccc aaaaccaaaa tccaaagttg 240
catggttttc caagtactta aacaaccctc taggaagggc tgtttctctt ctcgtcacac 300
tcacaatagg gtggcctatg tatttagcct tcaatgtctc tggtagaccc tatgatagtt 360
ttgcaagcca ctaccaccct tatgctccca tatattctaa ccgtgagagg cttctgatct 420
atgtctctga tgttgctttg ttttctgtga cttactctct ctaccgtgtt gcaaccctga 480
aagggttggt ttggctgcta tgtgtttatg gggtgccttt gctcattgtg aacggttttc 540
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aatgggactg gctgaaggga gctttggcaa ctatggacag agattaagcg ccgcatgcc   660
tccagaaaag aaagaaattt tcaagtcctt ggagggatgg cctcggagt gggtcctacc   720
gctgctgaag cccgtggagc aatgctggca gccacaaaac ttcctccctg accctccct   780
tccgcatgaa gagttcagcc atcaggtgaa ggagcttcgc gaacgcacta aagagttacc   840
tgatgagtac tttgtggtgc tggtgggtga tatggtcacc gaggacgcgc ttcccactta   900
ccagaccatg atcaacaacc ttgatggagt gaaagatgac agcggcacga gcccgagccc   960
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gagaagcttg aaggattgat gcctgagggg aagcgggccc caggatttcc gtgtgtgggt 1560
tgcccccgag gattaggagg ttccaagaac gcgctgatga gcgagcgcgt aagatgaaga 1620
agcatcatgc cgttaagttc agttggattt tcaataaaga attgcttttg tgagcggccg 1680
ccgactcgac gatgagcgag atgaccagct ccggccg   1717

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<210>   25
<211>   21
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence:  PCR primer for amplification
        of soybean Lea promoter 5'-end

<400>   25
attaacctca attcttctaa g                                                21


<210>   26
<211>   20
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence:  PCR primer for amplification
        of soybean Lea promoter 3'end

<400>   26
ttcaaagatc aattatttcc                                                  20


<210>   27
<211>   22
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence:  PCR primer for amplification
        of phaseolin terminator 5'-end

<400>   27
catggccacg tgcatgaagt at                                               22


<210>   28
<211>   22
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence:  PCR primer for amplification
        of phaseolin terminator 3'-end


<400>   28
atccctgaag tgtctcattt ta                                               22


<210>   29
<211>   963
<212>   DNA
<213>   Artificial Sequence
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<220>
<223> Description of Artificial Sequence: ELVISLIVES complementary
region of pKS149

<400> 29

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cggccggagc tggtcatctc gctcatcgtc gagtcggcgg ccgctgagct gatttaaatc   60
accactgtca aaaccaccat caccgacgct caagccaagg tcgccaccga tcatggtcgt  120
gcctacgtca ccttcctcgc cggaaacggt gactatgtga aaggtgtcgt tggcttggca  180
aaaggtctga gaaaagtgaa gagcatgtac cctctggtgg ttgcagtgct acccgatgtt  240
ccccaagatc accgcaacat tctcacctcc caaggttgca ttgttagaga gattgagccc  300
gtgtacccc cagagaatca aacccagttt gccatggcat attacgtcat caactattcc  360
aagctacgta tttgggagtt tgtggagtac agcaagatga tatacctaga cggtgatatc  420
caagttttg acaacattga ccacttggga tcgatcctga gctgatttaa accaccgttg  480
ttgccaatgt caccaccgag caattaccca aggctcgtgg aggaagtggg cgtgccttcg  540
tgacctttct tgctgggaac ggtgattacg taaagggtgt cgtgggtttg gccaaaggac  600
tgagaaaggc caaaagcatg tacccttttgg tggttgctgt gttaccagat gttcctgaag  660
aacatcgtga gattctcaaa tcccaaggtt gcattgtcag ggagattgaa cctgtgtacc  720
ctcctgagaa ccagacccag ttcgtcatgg cctattatgt catcaattac tccaagctac  780
gtatttggga gttcgtggag tacaagaaga cgatatacct agacggtgac atccaagtat  840
ttggaaacat agaccacttg tttgatctgt gagctgattt aagcggccgc cgactcgacg  900
atgagcgaga tgaccagctc cggccgccga ctcgacgatg agcgagatga ccagctccgg  960
ccg                                                                  963
```

<210> 30
<211> 987
<212> DNA
<213> Glycine max

<400> 30

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atggctccta atatcaccac tgtcaaaacc accatcaccg acgctcaagc caaggtcgcc   60
accgatcatg gtcgtgccta cgtcaccttc ctcgccggaa acggtgacta tgtgaaaggt  120
gtcgttggct tggcaaaagg tctgagaaaa gtgaagagca tgtaccctct ggtggttgca  180
gtgctacccg atgttcccca agatcaccgc aacattctca cctcccaagg ttgcattgtt  240
agagagattg agcccgtgta ccccccagag aatcaaaccc agtttgccat ggcatattac  300
gtcatcaact attccaagct acgtatttgg gagtttgtgg agtacagcaa gatgatatac  360
ctagacggtg atatccaagt ttttgacaac attgaccact tgtttgactt gcctgataac  420
tacttctatg cggtgatgga ctgtttctgt gagccaactt ggggccacac taaacaatat  480
cagatcggtt actgccagca gtgcccccat aaggttcagt ggcccactca ctttgggccc  540
aaacctcctc tctatttcaa tgctggcatg tttgtgtatg agcccaattt ggctacttac  600
cgtgacctcc ttcaaacagt ccaagtcacc cagcccactt cctttgctga acaggatttt  660
ttgaacatgt acttcaagga caaatatagg ccaattccta atgtctacaa tcttgtgctg  720
gccatgctgt ggcgtcaccc tgagaacgtt gagcttgaca aagttaaagt ggttcactac  780
tgtgctgctg ggtctaagcc ttggaggtac actgggaagg aggagaatat ggagagagaa  840
gatatcaaga tgttagtgaa aaagtggtgg gatatatatg aggatgagac tttggactac  900
aacaatccac tcaatgtgga taagttcact gcggcactta tggaggttgg tgaagtcaag  960
ttcgtccgtg ccccatctgc tgcttaa                                        987
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<210> 31
<211> 328
<212> PRT
<213> Glycine max

<400> 31

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Met Ala Pro Asn Ile Thr Thr Val Lys Thr Thr Ile Thr Asp Ala Gln
                  5                  10                  15

Ala Lys Val Ala Thr Asp His Gly Arg Ala Tyr Val Thr Phe Leu Ala
             20                  25                  30
```

8

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Gly Asn Gly Asp Tyr Val Lys Gly Val Val Gly Leu Ala Lys Gly Leu
        35                  40                  45

Arg Lys Val Lys Ser Met Tyr Pro Leu Val Val Ala Val Leu Pro Asp
    50                  55                  60

Val Pro Gln Asp His Arg Asn Ile Leu Thr Ser Gln Gly Cys Ile Val
65                  70                  75                  80

Arg Glu Ile Glu Pro Val Tyr Pro Pro Glu Asn Gln Thr Gln Phe Ala
                85                  90                  95

Met Ala Tyr Tyr Val Ile Asn Tyr Ser Lys Leu Arg Ile Trp Glu Phe
            100                 105                 110

Val Glu Tyr Ser Lys Met Ile Tyr Leu Asp Gly Asp Ile Gln Val Phe
            115                 120                 125

Asp Asn Ile Asp His Leu Phe Asp Leu Pro Asp Asn Tyr Phe Tyr Ala
    130                 135                 140

Val Met Asp Cys Phe Cys Glu Pro Thr Trp Gly His Thr Lys Gln Tyr
145                 150                 155                 160

Gln Ile Gly Tyr Cys Gln Gln Cys Pro His Lys Val Gln Trp Pro Thr
            165                 170                 175

His Phe Gly Pro Lys Pro Pro Leu Tyr Phe Asn Ala Gly Met Phe Val
            180                 185                 190

Tyr Glu Pro Asn Leu Ala Thr Tyr Arg Asp Leu Leu Gln Thr Val Gln
        195                 200                 205

Val Thr Gln Pro Thr Ser Phe Ala Glu Gln Asp Phe Leu Asn Met Tyr
    210                 215                 220

Phe Lys Asp Lys Tyr Arg Pro Ile Pro Asn Val Tyr Asn Leu Val Leu
225                 230                 235                 240

Ala Met Leu Trp Arg His Pro Glu Asn Val Glu Leu Asp Lys Val Lys
            245                 250                 255

Val Val His Tyr Cys Ala Ala Gly Ser Lys Pro Trp Arg Tyr Thr Gly
            260                 265                 270

Lys Glu Glu Asn Met Glu Arg Glu Asp Ile Lys Met Leu Val Lys Lys
        275                 280                 285

Trp Trp Asp Ile Tyr Glu Asp Glu Thr Leu Asp Tyr Asn Asn Pro Leu
    290                 295                 300

Asn Val Asp Lys Phe Thr Ala Ala Leu Met Glu Val Gly Glu Val Lys
305                 310                 315                 320

Phe Val Arg Ala Pro Ser Ala Ala
            325
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9

<210> 32
<211> 1350
<212> DNA
<213> Glycine max

<400> 32
gcacgagaaa caaccaacct cttcagtgat ctttgattag tactaagcta aaccatttct   60
tattccctca aaatcaaaac cttttctttt ctagctattt cccttttcaa atcatgccac   120
ctaacatcac caccgttgtt gccaatgtca ccaccgagca attacccaag gctcgtggag   180
gaagtgggcg tgccttcgtg acctttcttg ctgggaacgg tgattacgta aagggtgtcg   240
tgggtttggc caaaggactg agaaaggcca aagcatgta cccttttggtg gttgctgtgt   300
taccagatgt tcctgaagaa catcgtgaga ttctcaaatc ccaaggttgc attgtcaggg   360
agattgaacc tgtgtaccct cctgagaacc agacccagtt cgccatggcc tattatgtca   420
tcaattactc caagctacgt atttgggagt tcgtggagta caagaagacg atataccatg   480
acggtgacat ccaagtattt ggaaacatag accacttgtt tgatctgcct gataattatt   540
tctatgcggt gatggattgt ttctgcgaga agacttggag ccacaccect cagttccaga   600
ttgggtactg ccaacagtgc cctgataagg ttcaatggcc ctctcacttt ggttccaaac   660
ctcctctata tttcaatgct ggcatgtttg tttatgagcc taatctcgac acctaccgtg   720
atcttctcca aactgtccaa ctcaccaagc ccacttcttt tgctgagcag gactttctca   780
acatgtactt caaggacaag tacaagccaa taccgaacat gtacaacctt gtgctggcca   840
tgttgtggcg tcaccctgaa aatgttgaac ttgataaagt tcaagtggtt cattactgtg   900
ctgctgggtc taagccttgg aggttcactg ggaaggaaga gaacatggat agggaagata   960
tcaagatgct tgtgaagaag tggtggggaca tatatgaaga tgagacactg gactacaata   1020
acaactctgt caacgtggaa cgtttcacat cggcactatt ggatgctggg ggctttcagt   1080
ttgtgccagc accttctgct gcctaatatg cttattattt acagctacaa attaatgtta   1140
attaacgaca aagtatatgt attgttattt gctttttttc gttttttgggt cttatatatg   1200
aaggaacaac gtctatggtt ttaatttgga tgaccttctt gtatacaaag ccacatgtga   1260
tctcatacag cttttgatta ttattaagaa attagaggac cttttattat gagtcctta   1320
cttaaaaaaa aaaaaaaaaa aaaaaaaaa   1350

<210> 33
<211> 358
<212> PRT
<213> Glycine max

<400> 33
Ser Leu Ile Ser Thr Lys Leu Asn His Phe Leu Phe Pro Gln Asn Gln
  1   5   10   15

Asn Leu Phe Leu Ser Ser Tyr Phe Pro Phe Gln Ile Met Pro Pro Asn
             20   25   30

Ile Thr Thr Val Val Ala Asn Val Thr Thr Glu Gln Leu Pro Lys Ala
         35   40   45

Arg Gly Gly Ser Gly Arg Ala Phe Val Thr Phe Leu Ala Gly Asn Gly
     50   55   60

Asp Tyr Val Lys Gly Val Val Gly Leu Ala Lys Gly Leu Arg Lys Ala
 65   70   75   80

Lys Ser Met Tyr Pro Leu Val Val Ala Val Leu Pro Asp Val Pro Glu
                 85   90   95

Glu His Arg Glu Ile Leu Lys Ser Gln Gly Cys Ile Val Arg Glu Ile
             100   105   110

Glu Pro Val Tyr Pro Pro Glu Asn Gln Thr Gln Phe Ala Met Ala Tyr
             115   120   125

```
Tyr Val Ile Asn Tyr Ser Lys Leu Arg Ile Trp Glu Phe Val Glu Tyr
    130                 135             140

Lys Lys Thr Ile Tyr Leu Asp Gly Asp Ile Gln Val Phe Gly Asn Ile
145                 150             155                     160

Asp His Leu Phe Asp Leu Pro Asp Asn Tyr Phe Tyr Ala Val Met Asp
                165             170                 175

Cys Phe Cys Glu Lys Thr Trp Ser His Thr Pro Gln Phe Gln Ile Gly
            180             185             190

Tyr Cys Gln Gln Cys Pro Asp Lys Val Gln Trp Pro Ser His Phe Gly
        195             200             205

Ser Lys Pro Pro Leu Tyr Phe Asn Ala Gly Met Phe Val Tyr Glu Pro
    210             215             220

Asn Leu Asp Thr Tyr Arg Asp Leu Leu Gln Thr Val Gln Leu Thr Lys
225             230             235             240

Pro Thr Ser Phe Ala Glu Gln Asp Phe Leu Asn Met Tyr Phe Lys Asp
            245             250             255

Lys Tyr Lys Pro Ile Pro Asn Met Tyr Asn Leu Val Leu Ala Met Leu
            260             265             270

Trp Arg His Pro Glu Asn Val Glu Leu Asp Lys Val Gln Val Val His
        275             280             285

Tyr Cys Ala Ala Gly Ser Lys Pro Trp Arg Phe Thr Gly Lys Glu Glu
    290             295             300

Asn Met Asp Arg Glu Asp Ile Lys Met Leu Val Lys Lys Trp Trp Asp
305             310             315             320

Ile Tyr Glu Asp Glu Thr Leu Asp Tyr Asn Asn Asn Ser Val Asn Val
            325             330             335

Glu Arg Phe Thr Ser Ala Leu Leu Asp Ala Gly Gly Phe Gln Phe Val
        340             345             350

Pro Ala Pro Ser Ala Ala
        355


<210>   34
<211>   515
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence:  SHH3 complementary
        region of PHP17939

<400>   34
gttaacagct ttatttgttc taggttgttc atgaaatatt tttttggttt tatctccgtt   60
gtaagaaaat catgtgcttt gtgtcgccac tcactattgc agctttttca tgcattggtc  120
agattgacgg ttgattgtat ttttgttttt tatggttttg tgttatgact taagtcttca  180
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11

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tctctttatc tcttcatcag gtttgacggt tacttaatat ggtgcatgca tgggtacatc 240
actagaaacc atggaaggta ccaagatatc aaccgcggaa agatcgtaca aatggcatgt 300
taaataaccg tcaaacctga tgaagagata aagagatgaa gacttaagtc ataacacaaa 360
accataaaaa acaaaaatac aatcaaccgt caatctgacc aatgcatgaa aaagctgcaa 420
tagtgagtgg cgacacaaag cacatgattt tcttacaacg gagataaaac caaaaaaata 480
tttcatgaac aacctagaac aaataaagcg ttaac                             515
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<210> 35
<211> 1968
<212> DNA
<213> Glycine max

<400> 35
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ctcaccaaac ccaaccacgc tctcaaaatc aaatgttcca tctccaaacc ccccacggcg  180
gcgcccttca ccaaggaagc gccgaccacg gagcccttcg tgtcacggtt cgcctccggc  240
gaacctcgca agggcgcgga catccttgtg gaggcgctgg agaggcaggg cgtgacgacg  300
gtgttcgcgt accccggcgg tgcgtcgatg gagatccacc aggcgctcac gcgctccgcc  360
gccatccgca acgtgctccc gcgccacgag cagggcggcg tcttcgccgc cgaaggctac  420
gcgcgttcct ccggcctccc cggcgtctgc attgccacct ccggcccccgg cgccaccaac  480
ctcgtgagcg gcctcgccga cgctttaatg gacagcgtcc cagtcgtcgc catcaccggc  540
caggtcgccc gccggatgat cggcaccgac gccttccaag aaaccccgat cgtggaggtg  600
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